

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HOGREFE, Holly
HANSEN, Connie J

(ii) TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
Extracts, PEF Protein Complexes, Isolated PEF Proteins,
and Methods for Purifying and Identifying Them

(iii) NUMBER OF SEQUENCES: 89

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington

(D) STATE: DC

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 24-OCT-1997

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: KULIK, David J

(B) REGISTRATION NUMBER: 36,576

(C) REFERENCE/DOCKET NUMBER: 1486/43163cp

(ix) TELECOMMUNICATION INFORMATION:

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2025 OCT 24 10 49 AM '97

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa	Xaa	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Xaa	Xaa	Xaa
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Arg	Xaa	Glu	Xaa	Leu	Xaa	Xaa
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

2542007 6025580

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Leu Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Arg Xaa
1 5 10 15

Leu Val Gly Lys Xaa Ile Val Leu Ala Ile Pro Gly Xaa Xaa Ala Xaa
20 25 30

Xaa Xaa Xaa
35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Glu Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

264307 5025630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Tyr Asp Ala Val Ile Met Ala Ala Ala Val Val Asp Phe Arg Pro
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Xaa Lys Leu Arg
1 5 10 15

264497-5025880

Lys

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Xaa
1 5 10 15
Arg Lys

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

2595709-1592580

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly	Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Lys	Phe	Arg	Lys	Glu	Glu	Ser
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Ala	Ile	Leu	Leu	Pro	Asp	Trp	Lys	Ile	Arg	Lys	Glu	Ile	Leu	Ile
1				5					10					15	

Glu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

264201" 6025683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa	Met	His	His	Val	Ile	Lys	Leu	Xaa	Tyr	Ala	Thr	Xaa	Ser	Arg	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Leu	Tyr	Leu	Val	Arg	Pro	Asp	Trp	Lys	Arg	Arg	Lys	Glu	Ile	Leu
1				5					10					15	

Ile Glu

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAYCAYGAHA ARYTHATTTA CGC

23

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs

264334 " 5045680

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCATDATNA CDGCRTCGTA TTT

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAYCAYGAHA ARYTHATATA CGC

23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ARDACDACYT GRTTTTCTTC

20

23456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTTCACC	ACGTCAAGCT	AATCTACGCC	ACAAAAAGTC	GAAAGCTAGT	TGGAAAAAAG	60
ATAGTCNNNN	NNNNNCCAGG	GAGTATTGCG	GCTTTGGATG	TGAAAGCTTG	TGAGGGACTA	120
ATTAGGCATG	GGGCCGAAGT	TCATGCAGTG	ATGAGTGAGG	CAGCCACCAA	GATAATTCAT	180
CCTTATGCAT	GGAATTTGCC	CACGGGAAAT	CCAGTCATAA	CTGAGATCAC	TGGATTTATC	240
GAGCATGTTG	AGTTAGCAGG	GGAACATGAG	AATAAAGCAG	ATTTAATTTT	GGTTTGTCTT	300
GCCACTGCCA	ACACAATTAG	TAAGATTGCA	TGTGGAATAG	ATGATACTCC	AGTAACTACA	360
GTCGTGACCA	CAGCATTTCC	CCACATTCCA	ATTATGATAG	CCCCAGCAAT	GCATGAGACA	420
ATGTACAGGC	ATCCCATAGT	AAGGGAGAAC	ATTGAAAGGT	TAAAGAAGCT	TGGCGTTGAG	480
TTTATAGGAC	CAAGAATTGA	GGAGGGAAAG	GCAAAAAGTTG	CAAGCATTGA	TGAAATAGTT	540
TACAGAGTTA	TTAAAAAGCT	CCACAAAAAA	ACATTGGAAG	GGAAGAGAGT	CCTAGTAACG	600
GCGGGAGCAA	CAAGAGAGTA	CATAGATCCA	ATAAGATTCA	TAACAAATGC	CAGCAGTGGA	660
AAAATGGGAG	TAGCGTTGGC	TGAAGAAGCA	GATTTTAGAG	GAGCTGTTAC	CCTCATAAGA	720
ACAAAGGGAA	GTGTAAAGGC	TTTTAGAATC	AGAAAAATCA	AATTGAAGGT	TGAGACAGTG	780
GAAGAAATGC	TTTCAGCGAT	TGAAAATGAG	TTGAGGAGTA	AAAAGTATGA	CGTAGTTATT	840
ATGGCAGCTG	CTGTAAGCGA	TTTLAGGCCA	AAAATTAAAG	CAGAGGGAAA	AATTAAAAGC	900
GGAAGATCAA	TAACGATAGA	GCTCGTTCCN	NNNAATCCCA	AAATCATTGA	TAGAATAAAG	960
GAAATTCAAC	CAAATGTCTT	TCTTGTGGA	TTTAAAGCAG	AAACTTCAAA	AGAAAAGCTT	1020
ATAGAAGAAG	GTAAAAGGCA	GATTGAGAGG	GCCAAGGCTG	ACTTAGTCGT	TGGTAACACA	1080
TTGGAAGCCT	TTGGAAGCGA	GGAAAACCAA	GTAGTATTAA	TTGGCAGAGA	TTTCACAAAA	1140

GAAGTTCCAA AAATGAAAAA GAGAGAGTTA GCAGAGAGAA TTTGGGATGA GATAGAGAAA 1200
TTNCTGTCC 1209

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Lys	Ser	Arg	Lys	Leu	1	5	10	15
Val	Gly	Lys	Lys	Ile	Val	Xaa	Xaa	Xaa	Pro	Gly	Ser	Ile	Ala	Ala	Leu	20	25	30	
Asp	Val	Lys	Ala	Cys	Glu	Gly	Leu	Ile	Arg	His	Gly	Ala	Glu	Val	His	35	40	45	
Ala	Val	Met	Ser	Glu	Ala	Ala	Thr	Lys	Ile	Ile	His	Pro	Tyr	Ala	Trp	50	55	60	
Asn	Leu	Pro	Thr	Gly	Asn	Pro	Val	Ile	Thr	Glu	Ile	Thr	Gly	Phe	Ile	65	70	75	80
Glu	His	Val	Glu	Leu	Ala	Gly	Glu	His	Glu	Asn	Lys	Ala	Asp	Leu	Ile	85	90	95	
Leu	Val	Cys	Pro	Ala	Thr	Ala	Asn	Thr	Ile	Ser	Lys	Ile	Ala	Cys	Gly	100	105	110	
Ile	Asp	Asp	Thr	Pro	Val	Thr	Thr	Val	Val	Thr	Thr	Ala	Phe	Pro	His	115	120	125	
Ile	Pro	Ile	Met	Ile	Ala	Pro	Ala	Met	His	Glu	Thr	Met	Tyr	Arg	His	130	135	140	
Pro	Ile	Val	Arg	Glu	Asn	Ile	Glu	Arg	Leu	Lys	Lys	Leu	Gly	Val	Glu	145	150	155	160
Phe	Ile	Gly	Pro	Arg	Ile	Glu	Glu	Gly	Arg	Ala	Lys	Val	Ala	Ser	Ile	165	170	175	
Asp	Glu	Ile	Val	Tyr	Arg	Val	Ile	Lys	Lys	Leu	His	Lys	Lys	Thr	Leu	180	185	190	
Glu	Gly	Lys	Arg	Val	Leu	Val	Thr	Ala	Gly	Ala	Thr	Arg	Glu	Tyr	Ile				

264307 15022588

195

200

205

Asp Pro Ile Arg Phe Ile Thr Asn Ala Ser Ser Gly Lys Met Gly Val
 210 215 220
 Ala Leu Ala Glu Glu Ala Asp Phe Arg Gly Ala Val Thr Leu Ile Arg
 225 230 235 240
 Thr Lys Gly Ser Val Lys Ala Phe Arg Ile Arg Lys Ile Lys Leu Lys
 245 250 255
 Val Glu Thr Val Glu Glu Met Leu Ser Ala Ile Glu Asn Glu Leu Arg
 260 265 270
 Ser Lys Lys Tyr Asp Val Val Ile Met Ala Ala Ala Val Ser Asp Phe
 275 280 285
 Arg Pro Lys Ile Lys Ala Glu Gly Lys Ile Lys Ser Gly Arg Ser Ile
 290 295 300
 Thr Ile Glu Leu Val Pro Xaa Asn Pro Lys Ile Ile Asp Arg Ile Lys
 305 310 315 320
 Glu Ile Gln Pro Asn Val Phe Leu Val Gly Phe Lys Ala Glu Thr Ser
 325 330 335
 Lys Glu Lys Leu Ile Glu Glu Gly Lys Arg Gln Ile Glu Arg Ala Lys
 340 345 350
 Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
 355 360 365
 Asn Gln Val Val Leu Ile Gly Arg Asp Phe Thr Lys Glu Leu Pro Lys
 370 375 380
 Met Lys Lys Arg Glu Leu Ala Glu Arg Ile Trp Asp Glu Ile Glu Lys
 385 390 395 400
 Xaa Leu Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATAGCGAAT TCGCAAAACC TTTCGCGGTA TGG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTACGGAAT TCCACGGAAA ATGCCGCTCA TCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCGTTTCCG TTCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

264204-604580

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATCTCACG CGCCAGTTTC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTTGCTC AACTTTATC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATAGAGATA GTTCTGGAG ACG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGATATCG ACATTCTGC ACC

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGACTCAG AAGCTGCTAT CGAA

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCACGTGC CCTGTAGGAT TTGT

24

24252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCAGAYTGGA ARWKNAGGAA AGA

23

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGAYTGGA ARWKNAGAAA AGA

23

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAGAYTGGA ARWKNAGGAA GGA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAYTGGA ARWKNAGAAA GGA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGAGTGGGC AGAGAGGCTN TTGTTAAGGG GAAATTAATC GACGTGGAAA
AGGAAGGAAA 60

AGTCGNTATT CCTCCAAGGG AATA

84

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Trp Ala Glu Arg Leu Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys
1 5 10 15

Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Val Gly Arg Glu Ala Xaa Val Lys Gly Lys Leu Ile Glu Val Glu
1 5 10 15

Lys Glu Gly Lys Val Xaa Ile Pro Pro Arg Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gln Ser Gly Gln Arg Gly Xaa Cys Xaa Gly Glu Ile Asn Arg Ser Gly
1 5 10 15

Lys Gly Arg Lys Ser Arg Tyr Ser Ser Lys Gly Leu
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCCCACTC TGAGGTCATA ACCTGCTGGT TGGAGCCATT CTTCAGAAAA TGGCTCTATA 60
AGTATTTCTT TTCTGATTTT CCAGTCTGGA AGTAGCATTT TACCACCGAA ACCTTTATTT 120
TTAATTTAA 129

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Xaa Ile Lys Asn Lys Gly Phe Gly Gly Lys Met Leu Leu Pro Asp Trp
1 5 10 15

Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro Phe Ser Glu Glu Trp Leu
 20 25 30
 Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCTCCAAGG GAATACGCCT TAATCCTAAC CCTCGAGAGG ATAAAGTTGC CCGACGATGT	60
TATGGGGGAT ATGAAGATAA GGAGCAGTTT AGCAAGAGAA GGGGTTATTG GTTCTTTTGC	120
TTGGGTTGAC CCAGGATGGG ATGGAAACTT AACACTAATG CTCTACAATG CCTCAAATGA	180
ACCTGTGCGAA TTAAGATATG GAGAGAGATT TGTGCAGATC GCATTTATAA GGCTAGAGGG	240
TCCGGCAAGA AACCCCTTACA GAGGAAACTA TCAGGGGAGC ACAAGGTTAG CGTTTTCAAA	300
GAGAAAGAAA CTCTAGCGTC TTTTCAATAG CATCCTCAAT ATCTCGTGTG AAGTAATCAA	360
TGTAAATACT TGCTGGGTGG GTTTTTAGGG ATTCAAATC GTAAGATGGG CCTGTATAGC	420
AGAAAACTAT TTTTGCCTCT TCTTCATTTA TCTTTCTGTG AATAAAAAAT CCAACATCCA	480
CACTAGTTCC AAAAGATATT GTTTGCGTGA TTACCAACAA GATCTTGGCA TTATTTTGA	540
TCTTATACTC TATTCTCCTT TCTCCCTCCA ATTTGCCCAA AATAAACCTG GGTAGTATAC	600
ATTCACCTCT CTCTTTTAAA TTCCTATAAA TTCGTACATA GTTTAGAAAA ATGTCAAATT	660
CTTNTTCCC TGTTAAATTA ACCNCNAAAT CTTTATNANN AANCTTTTTA TAATTCCCAA	720
AACCCCTAAT TTTCCCCTTN	740

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Leu	Gln	Gly	Asn	Thr	Pro	Xaa	Ser	Xaa	Pro	Ser	Arg	Gly	Xaa	Ser	Cys
1				5					10					15	
Pro	Thr	Met	Leu	Trp	Gly	Ile	Xaa	Arg	Xaa	Gly	Ala	Val	Xaa	Gln	Glu
			20					25					30		
Lys	Gly	Leu	Leu	Val	Leu	Leu	Leu	Gly	Leu	Thr	Gln	Asp	Gly	Met	Glu
		35					40					45			
Thr	Xaa	His	Xaa	Cys	Ser	Thr	Met	Pro	Gln	Met	Asn	Leu	Ser	Asn	Xaa
	50					55					60				
Asp	Met	Glu	Arg	Asp	Leu	Cys	Arg	Ser	His	Leu	Xaa	Gly	Xaa	Arg	Val
65					70					75				80	
Arg	Gln	Glu	Thr	Leu	Thr	Glu	Glu	Thr	Ile	Arg	Gly	Ala	Gln	Gly	Xaa
				85					90					95	
Arg	Phe	Gln	Arg	Glu	Arg	Asn	Ser	Ser	Val	Phe	Ser	Ile	Ala	Ser	Ser
			100					105					110		
Ile	Ser	Arg	Val	Lys	Xaa	Ser	Met	Xaa	Ile	Leu	Ala	Gly	Trp	Val	Phe
		115					120					125			
Arg	Asp	Ser	Asn	Ser	Xaa	Asp	Gly	Pro	Val	Xaa	Gln	Lys	Thr	Ile	Phe
	130					135					140				
Ala	Ser	Ser	Ser	Phe	Ile	Phe	Leu	Xaa	Ile	Lys	Asn	Pro	Thr	Ser	Thr
145					150					155					160
Leu	Val	Pro	Lys	Asp	Ile	Val	Cys	Val	Ile	Thr	Asn	Lys	Ile	Leu	Ala
			165						170					175	
Leu	Phe	Leu	Ile	Leu	Tyr	Ser	Ile	Leu	Leu	Ser	Pro	Ser	Asn	Leu	Pro
		180						185					190		
Lys	Ile	Asn	Leu	Gly	Ser	Ile	His	Ser	Leu	Leu	Ser	Phe	Lys	Phe	Leu
	195						200					205			
Xaa	Ile	Arg	Thr	Xaa	Phe	Arg	Lys	Met	Ser	Asn	Ser	Xaa	Phe	Pro	Val
	210					215					220				

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Lys Leu Thr Xaa Lys Ser Leu Xaa Xaa Xaa Phe Leu Xaa Phe Pro Lys
 225 230 235 240

Pro Leu Ile Phe Pro Xaa
 245

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu Arg Ile Lys Leu
 1 5 10 15

Pro Asn Asn Val Met Gly Asp Met Lys Ile Arg Ser Ser Leu Ala Arg
 20 25 30

Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro Gly Trp Asp Gly
 35 40 45

Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu Pro Val Glu Leu
 50 55 60

Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile Arg Leu Glu Gly
 65 70 75 80

Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly Ser Thr Arg Leu
 85 90 95

Ala Phe Ser Lys Arg Lys Lys Leu Xaa Arg Leu Phe Asn Ser Ile Leu
 100 105 110

Asn Ile Ser Cys Glu Val Ile Asn Val Asn Thr Cys Trp Val Gly Phe
 115 120 125

Xaa Gly Phe Lys Leu Val Arg Trp Ala Cys Ile Ala Glu Asn Tyr Phe
 130 135 140

Cys Leu Phe Phe Ile Tyr Leu Ser Val Asn Lys Lys Ser Asn Ile His
 145 150 155 160

Thr Ser Ser Lys Arg Tyr Cys Leu Arg Asp Tyr Gln Gln Asp Leu Gly
 165 170 175

Ile Ile Phe Asp Leu Ile Leu Tyr Ser Pro Phe Ser Leu Gln Phe Ala
 180 185 190

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Gln Asn Lys Pro Gly Xaa Tyr Thr Phe Thr Pro Leu Phe Xaa Ile Pro
195 200 205

Ile Asn Ser Tyr Ile Val Xaa Lys Asn Val Lys Phe Phe Xaa Pro Cys
210 215 220

Xaa Ile Asn Xaa Xaa Ile Phe Xaa Xaa Xaa Leu Phe Ile Ile Pro Lys
225 230 235 240

Thr Pro Asn Phe Pro Leu
245

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Lys Gly Ile Arg Leu Asn Pro Asn Pro Arg Glu Asp Lys Val
1 5 10 15

Ala Arg Arg Cys Tyr Gly Gly Tyr Glu Asp Lys Glu Gln Phe Ser Lys
20 25 30

Arg Arg Gly Tyr Trp Phe Phe Cys Leu Gly Xaa Pro Arg Met Gly Trp
35 40 45

Lys Leu Asn Thr Asn Ala Leu Gln Cys Leu Lys Xaa Thr Cys Arg Ile
50 55 60

Lys Ile Trp Arg Glu Ile Cys Ala Asp Arg Ile Tyr Lys Ala Arg Gly
65 70 75 80

Ser Gly Lys Lys Pro Leu Gln Arg Lys Leu Ser Gly Glu His Lys Val
85 90 95

Ser Val Phe Lys Glu Lys Glu Thr Leu Ala Ser Phe Gln Xaa His Pro
100 105 110

Gln Tyr Leu Val Xaa Ser Asn Gln Cys Lys Tyr Leu Leu Gly Gly Phe
115 120 125

Leu Gly Ile Gln Thr Arg Lys Met Gly Leu Tyr Ser Arg Lys Leu Phe
130 135 140

Leu Pro Leu Leu His Leu Ser Phe Cys Glu Xaa Lys Ile Gln His Pro
145 150 155 160

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His Xaa Phe Gln Lys Ile Leu Phe Ala Xaa Leu Pro Thr Arg Ser Trp
165 170 175

His Tyr Phe Xaa Ser Tyr Thr Leu Phe Ser Phe Leu Pro Pro Ile Cys
180 185 190

Pro Lys Xaa Thr Trp Val Val Tyr Ile His Ser Ser Leu Leu Asn Ser
195 200 205

Tyr Lys Phe Val His Ser Leu Glu Lys Cys Gln Ile Leu Xaa Ser Leu
210 215 220

Leu Asn Xaa Pro Xaa Asn Leu Tyr Xaa Xaa Xaa Phe Tyr Asn Ser Gln
225 230 235 240

Asn Pro Xaa Phe Ser Pro
245

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Ser Arg Lys Leu
1 5 10 15

Val Gly Lys Lys Ile Val Xaa Xaa Xaa Pro Gly Ser Ile Ala Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

264204 5025680

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Tyr Asp Val Val Ile Met Ala Ala Val Ser Asp Phe Arg Phe
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg
20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

264207 60225630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Methanococcus Jannaschii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ile Ser Glu Ile Met His Pro Thr Lys Leu Leu Lys Gly Thr Lys
1 5 10 15

Ser Lys Leu Leu Glu Asn Lys Lys Ile Leu Val Ala Val Thr Ser Ser
20 25 30

Ile Ala Ala Ile Glu Thr Pro Lys Leu Met Arg Glu Leu Ile Arg His
35 40 45

Gly Ala Glu Val Tyr Cys Ile Ile Thr Glu Glu Thr Lys Lys Ile Ile
50 55 60

Gly Lys Glu Ala Leu Lys Phe Gly Cys Gly Asn Glu Val Tyr Glu Glu

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65

70

75

80

Ile Thr Gly Xaa Xaa Xaa Xaa Xaa Asp Ile Glu His Ile Leu Leu Tyr
85 90 95

Xaa Xaa Xaa Xaa Asn Glu Cys Asp Cys Leu Leu Ile Tyr Pro Ala Thr
100 105 110

Ala Asn Ile Ile Ser Lys Ile Asn Leu Gly Ile Ala Asp Asn Ile Val
115 120 125

Asn Thr Thr Ala Leu Met Phe Phe Gly Asn Lys Pro Ile Phe Ile Val
130 135 140

Pro Ala Met His Glu Asn Met Phe Asn Xaa Xaa Ala Ile Lys Arg His
145 150 155 160

Ile Asp Lys Leu Lys Glu Lys Asp Lys Ile Tyr Ile Ile Ser Pro Lys
165 170 175

Phe Glu Glu Xaa Xaa Xaa Xaa Xaa Xaa Gly Lys Ala Lys Val Ala Asn
180 185 190

Ile Glu Asp Val Val Lys Ala Val Ile Glu Lys Ile Gly Asn Asn Leu
195 200 205

Lys Lys Glu Gly Asn Arg Val Leu Ile Leu Asn Gly Gly Thr Val Glu
210 215 220

Phe Ile Asp Lys Val Arg Val Ile Ser Asn Leu Ser Ser Gly Lys Met
225 230 235 240

Gly Val Ala Leu Ala Glu Ala Phe Cys Lys Glu Gly Phe Tyr Val Glu
245 250 255

Val Ile Thr Ala Met Gly Leu Glu Pro Pro Tyr Tyr Ile Lys Asn His
260 265 270

Lys Val Leu Thr Ala Lys Glu Met Leu Asn Lys Ala Ile Glu Xaa Xaa
275 280 285

Leu Xaa Ala Lys Asp Phe Asp Ile Ile Ile Ser Ser Ala Ala Ile Ser
290 295 300

Asp Phe Thr Val Glu Ser Xaa Phe Glu Gly Lys Leu Ser Ser Glu Glu
305 310 315 320

Glu Xaa Xaa Xaa Xaa Leu Ile Leu Lys Leu Lys Arg Xaa Asn Pro Lys
325 330 335

Val Leu Glu Glu Leu Arg Arg Ile Tyr Lys Asp Xaa Lys Val Ile Ile
340 345 350

Gly Phe Lys Ala Glu Tyr Asn Leu Asp Glu Lys Glu Leu Ile Asn Arg
355 360 365

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Ala Lys Glu Arg Leu Asn Lys Tyr Asn Leu Asn Met Ile Ile Ala Asn
 370 375 380

Asp Leu Ser Lys Xaa Xaa His Tyr Phe Gly Asp Asp Tyr Ile Glu Val
 385 390 395 400

Tyr Ile Ile Thr Lys Tyr Glu Val Glu Lys Ile Ser Gly Ser Lys Lys
 405 410 415

Xaa Glu Ile Ser Glu Arg Ile Val Glu Lys Val Lys Lys Leu Val Lys
 420 425 430

Ser Xaa Xaa Xaa Xaa
 435

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ala Arg Gln Gln Lys Tyr Cys Asp Lys Ile Ala Asn Phe Trp
 1 5 10 15

Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile
 20 25 30

Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu
 35 40 45

Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr
 50 55 60

Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser
 65 70 75 80

Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala
 85 90 95

Met Gly His Ile Glu Leu Gly Xaa Xaa Xaa Xaa Lys Trp Ala Asp Leu
 100 105 110

Val Ile Leu Ala Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala

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115

120

125

Gly Met Ala Asn Asp Leu Val Ser Thr Ile Cys Leu Ala Thr Pro Xaa
130 135 140

Xaa Ala Pro Val Ala Val Leu Pro Ala Met Asn Gln Gln Met Tyr Arg
145 150 155 160

Ala Ala Ala Thr Gln His Asn Leu Glu Val Leu Ala Xaa Ser Arg Gly
165 170 175

Leu Leu Ile Trp Gly Pro Asp Ser Gly Ser Gln Ala Cys Gly Asp Ile
180 185 190

Gly Pro Gly Arg Xaa Xaa Asp Pro Leu Thr Ile Val Asp Met Ala Val
195 200 205

Ala His Phe Ser Pro Val Asn Asp Leu Lys His Leu Asn Ile Met Ile
210 215 220

Thr Ala Gly Pro Thr Arg Glu Pro Leu Asp Pro Val Arg Tyr Ile Ser
225 230 235 240

Asn His Ser Ser Gly Lys Met Gly Phe Ala Ile Ala Ala Ala Ala Ala
245 250 255

Arg Arg Gly Ala Asn Val Thr Leu Val Ser Gly Pro Val Ser Leu Pro
260 265 270

Thr Pro Pro Phe Val Lys Arg Val Asp Val Met Thr Ala Leu Glu Met
275 280 285

Glu Ala Ala Val Asn Xaa Xaa Ala Ser Val Gln Gln Gln Asn Ile Phe
290 295 300

Ile Gly Cys Ala Ala Val Ala Asp Tyr Arg Ala Ala Thr Val Ala Pro
305 310 315 320

Glu Lys Ile Lys Lys Gln Ala Thr Gln Gly Asp Glu Leu Thr Ile Lys
325 330 335

Met Val Lys Xaa Asn Pro Asp Ile Val Ala Gly Val Ala Ala Leu Lys
340 345 350

Asp His Arg Pro Tyr Val Val Gly Phe Ala Ala Glu Thr Asn Asn Xaa
355 360 365

Xaa Xaa Xaa Val Glu Glu Tyr Ala Arg Gln Lys Arg Ile Arg Lys Asn
370 375 380

Leu Asp Leu Ile Cys Ala Asn Asp Val Ser Gln Pro Thr Gln Gly Phe
385 390 395 400

Asn Ser Asp Asn Asn Ala Leu His Leu Phe Trp Gln Asp Gly Asp Lys
405 410 415

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Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu Leu Asp
420 425 430

Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg
435 440

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

25423015057500

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

08957091049
464207 6075680

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

46420T " 5025680

CAGGACTCAG AAGCTGCTAT CGAA

24

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGCACGTGC CCTGTAGGAT TTGT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

24252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

0895709-103497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

His His Val Lys Leu Ile Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Tyr Asp Ala Val Ile Met Ala
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Gln Val Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

264201 502530

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Pro Asp Trp Lys Ile Arg Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGCTACTTC CAGACTGGAA AATCAGAAAA GAAATACTTA TAGAGCCATT TTCTGAAGAA 60
TCGCTCCAAC CAGCAGGTTA TGACCTCAGA GTGGGCAGAG AGGCTTTTGT TAAGGGGAAA 120
TTAATCGACG TGGAAAAGGA AGGAAAAGTC GTTATTCCTC CAAGGGAATA CGCCTTAATC 180
CTAACCCCTCG AGAGGATAAA GTTGCCCGAC GATGTTATGG GGGATATGAA GATAAGGAGC 240
AGTTTAGCAA GAGAAGGGGT TATTGGTTCT TTTGCTTGGG TTGACCCAGG ATGGGATGGA 300
AACTTAACAC TAATGCTCTA CAATGCCTCA AATGAACCTG TCGAATTAAG ATATGGAGAG 360
AGATTGTGTC AGATCGCATT TATAAGGCTA GAGGGTCCGG CAAGAAACCC TTACAGAGGA 420
AACTATCAGG GGAGCACAAG GTTAGCGTTT TCAAAGAGAA AGAAACTCTA G 471

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Leu Leu Pro Asp Trp Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro
1 5 10 15
Phe Ser Glu Glu Ser Leu Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
20 25 30
Arg Glu Ala Phe Val Lys Gly Lys Leu Ile Asp Val Glu Lys Glu Gly
35 40 45
Lys Val Val Ile Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu
50 55 60
Arg Ile Lys Leu Pro Asp Asp Val Met Gly Asp Met Lys Ile Arg Ser
65 70 75 80
Ser Leu Ala Arg Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro
85 90 95
Gly Trp Asp Gly Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu
100 105 110
Pro Val Glu Leu Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile
115 120 125
Arg Leu Glu Gly Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly
130 135 140
Ser Thr Arg Leu Ala Phe Ser Lys Arg Lys Lys Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

085709-102497

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

264207" 60225680

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu Met Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Gly Val Val Asp Arg Asp Tyr Thr Gly Glu Val Lys Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20250910 10:24:49

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Gly Val Ile Asp Glu Asp Tyr Arg Gly Asn Val Gly Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Gly Leu Ile Asp Pro Gly Phe Gln Gly Glu Leu Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACGACGACA AGATGCTACT TCCAGACTGG AAA

33

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

2642007 " 50225630

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGAACAAGAC CCGTCCCACT TTCACAGATG AAGAG

35

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTCCATGTCC CAACTCCGAT CAC

23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTTTTCCCA GTCACGACGT TGTAACACGA CGGCCAGT

38

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGUUUCCCA GUCACGACGU UGUAAACGA CGGCCAGU

38

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACGACGACA AGATGCCCTG CTCTGAAGAG ACACC

35

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

264201 502580

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGAACAAGAC CCGTTTAATT CTTTCAGTG GAACC

35

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